

Serial No. 09/687,276.

Applicant(s): Prayaga *et al.*

Length = 1004

Score = 3036 bits (7128), Expect = 0.0

Identities = 945/992 (95%), Positives = 964/992 (96%), Gaps = 1/992 (0%)

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NOV2: 1 MAPARGRLPPALWVVTAATAAATCVSAARGEVNLLDTSTIHGDWGWLTYPAHGWDSINEV 60
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1 MAPARARLSPALWVVTAATAAATCVSAGRGEVNLLDTSTIHGDWGWLTYPAHGWDSINEV 59

NOV2: 61 DESFQPIHTYQVCNVMSPNQNNWLRTSWVPRDGARRVYAEIKFTLRDCNSMPGVLTCKE 120
      |||||+|||+|||+|||+|||+|||+|||+|||+|||+|||+|||+|||+|||+|||
Sbjct: 60 DESFRPIHTYQVCNVMSPNQNNWLRTNWVPRDGARRVYAEIKFTLRDCNSIPGVLTCKE 119

NOV2: 121 TFNLYYLESDRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTEVRSVGPLSKRG 180
      |||||+|||+|||+|||+|||+|||+|||+|||+|||+|||+|||+|||+|||+|||
Sbjct: 120 TFNLHYLESDDRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTEVRGVGPLSKRG 179

NOV2: 181 FYLAFQDIGACLAILSLRIYKKCPAMVRNLAAFSEAVTGADSSSLVEVRGQCVRHSEER 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 180 FYLAFQDIGACLAILSLRIYKKCPAMVRNLAAFSEAVTGADSSSLVEVRGQCVRHSEER 239

NOV2: 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACVACELGFYKSAPGDQLCARCPPHSHA 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 240 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACMACELGFYKSAPGDQLCARCPPHSHA 299

NOV2: 301 APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISVNGTSVTLEWAPPLDPGGRSDI 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 300 TPAAQTCRCDLSYYRAALDPSSAACTRPPSAPVNLISVNGTSVTLEWAPPLDPGGRSDI 359

NOV2: 361 TYNVAVCRRCPWALSRCEACGSGTRFVPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 360 TYNVAVCRRCPWALSHCEACGSGTRFVPQQTSLAQASLLVANLLAHMNYSFWIEAVNGVSN 419

NOV2: 421 LSPEPRRAAVVNITTNQAAPSQVVVIRQERAGQTSVSLWQEPNGIILEYEIKYYEK 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 420 LSPEPRSAAVVNITTNQAAPSQVVVIRQERAGQTSVSLWQEPNGIILEYEIKYYEK 479

NOV2: 481 DKEMQSYSTLKAVTTRATVSGLKPGTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 480 DKEMQSYSTLKAVTTRATVSGLKPGTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 539

NOV2: 541 RTIVWICLTLITGLVLLLLLLICKKRHCYGSKAFQDSDEEKMHYQNGQAPPPVFLPLHHP 600
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 540 RTIVWICLTLITGLVLLLLLLICKKRHCYGSKAFQDSDEEKMHYQNGQAPPPVFLPLNHP 599

NOV2: 601 PGKLPEPQFYAEPHTYEEPGRAGRSFTREIEASRIHIEKIIGSGDSGEVCYGRLRVPGQR 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 600 PGKFPETQFSAEPHTYEEPGRAGRSFTREIEASRIHIEKIIGSGESGEVCYGRQLQVPGQR 659

NOV2: 661 DVPVAIKALKAGYTERQRRDFLSEASIMQFDHPNIIIRLEGVVTRGRLAMIVTEYMENG 720
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 660 DVPVAIKALKAGYTERQRQDFLSEAAIMQFDHPNIIIRLEGVVTRGRLAMIVTEYMENG 719

NOV2: 721 LDTFLRTHDGQFTIMQLVGMLRGVAGMRYLSDLGYVHRDLAARNVLVDNLVCKVSDFG 780
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 720 LDAFLRTHDGQFTIVQLVGMLRGVAGMRYLSDLGYIHRDLAARNVLVDGRLVCKVSDFG 779

NOV2: 781 LSRVLEDDPDAAAYTTTGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 840
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 780 LSRALEDDPEAAAYTTTAGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 839

NOV2: 841 NMTNRDVISSVEEGYRLPAPMGCPRALHQLMLDCWHKDRAQRPRFSQIVSVLDALIRSPE 900
      |||||+|||+|||+|||+|||+|||+|||+|||+|||+|||+|||+|||+|||+|||
Sbjct: 840 NMTNQDVISSVEEGYRLPAPMGCPRALHQLMLDCWHKDRAQRPRFAHVSVLDALVHSPE 899

NOV2: 901 SLRATATVSRCPPPAFVRSCTDLRGGSGGGGGLTVGDWLD SIRMGRYRDHFAAGGYSSLG 960
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Sbjct: 900 SLRATATVSRCPPPAFARSCFDLRAGGSGNGDLTVGDWLD SIRMGRYRDHFAAGGYSSLG 959
NOV2: 961 MVLRMNAQDVRALGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:5)
|||||
Sbjct: 960 MVLRMNAQDVRALGITLMGHQKKILGSIQTMR 991 (SEQ ID NO:52)

Beginning on page 14, please replace Table 6A with the following Table 6A:

Table 6A.

Comparison between a NOV2 polypeptide and human ephrin receptor EphA8

>ref|NP_065387.1| EphA8; Ephrin receptor EphA8 (eph- and elk-related kinase); Hek3;
eph-, elk-related tyrosine kinase; ephrin receptor EphA8
emb|CAB81612.1| (AL035703) dJ61A9.1 (tyrosine kinase) [Homo sapiens]
Length = 1005

Score = 2054 bits (5262), Expect = 0.0
Identities = 992/992 (100%), Positives = 992/992 (100%)

NOV2 : 1 MAPARGRLPPALWVVTAATAAATCVSAARGEVNLLDTSTIHGDWGWLTPAHGWDSINEV 60
|||||
Sbjct: 1 MAPARGRLPPALWVVTAATAAATCVSAARGEVNLLDTSTIHGDWGWLTPAHGWDSINEV 60

NOV2 : 61 DESFQPIHTYQVCNVMSPNQNNWLRTSWVPRDGARRVYAEIKFTLRDCNSMPGVLGTCKE 120
|||||
Sbjct: 61 DESFQPIHTYQVCNVMSPNQNNWLRTSWVPRDGARRVYAEIKFTLRDCNSMPGVLGTCKE 120

NOV2 : 121 TFNLYYLESRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTEVRSVGPLSKRG 180
|||||
Sbjct: 121 TFNLYYLESRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTEVRSVGPLSKRG 180

NOV2 : 181 FYLAFQDIGACLA LSLRIYK KCPAMVRNLA AFSEAVTGADSSSLVEVRGQCVRHSEER 240
|||||
Sbjct: 181 FYLAFQDIGACLA LSLRIYK KCPAMVRNLA AFSEAVTGADSSSLVEVRGQCVRHSEER 240

NOV2 : 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACVACELGFYKSAPGDQLCARCPPHSHA 300
|||||
Sbjct: 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACVACELGFYKSAPGDQLCARCPPHSHA 300

NOV2 : 301 APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISVNGTSVTLEWAPPLDPGGRSDI 360
|||||
Sbjct: 301 APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISVNGTSVTLEWAPPLDPGGRSDI 360

NOV2 : 361 TYNVAVCRCPWALS RCEACGSGTRFVPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420
|||||
Sbjct: 361 TYNVAVCRCPWALS RCEACGSGTRFVPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420

NOV2 : 421 LSPEPRRAAVVNITTNQAAPSQVVVIRQERAGQTSVSLWQEPEQPNGIILEYEIKYYEK 480
|||||
Sbjct: 421 LSPEPRRAAVVNITTNQAAPSQVVVIRQERAGQTSVSLWQEPEQPNGIILEYEIKYYEK 480

NOV2 : 481 DKEMQSYSTLKA VTTTRATVSGLKPGTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540
|||||
Sbjct: 481 DKEMQSYSTLKA VTTTRATVSGLKPGTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540

NOV2 : 541 RTIVWICLTLITGLVVL LLLICKKRHCGYSKAFQDSDEEKMHYQNGQAPPPVFLPLHHP 600
|||||
Sbjct: 541 RTIVWICLTLITGLVVL LLLICKKRHCGYSKAFQDSDEEKMHYQNGQAPPPVFLPLHHP 600

NOV2 : 601 PGKLPEPQFYAEPHTYEEPGRAGRSFTREIEASRIHIEKIIGSGDSGEVCYGRRLRVPGQR 660
|||||
Sbjct: 601 PGKLPEPQFYAEPHTYEEPGRAGRSFTREIEASRIHIEKIIGSGDSGEVCYGRRLRVPGQR 660

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NOV2 : 661 DVPVAIKALKAGYTERQRRDFLSEASIMGQFDHPNIIIRLEGVVTRGRLAMIVTEYMENG 720
|||||
Sbjct: 661 DVPVAIKALKAGYTERQRRDFLSEASIMGQFDHPNIIIRLEGVVTRGRLAMIVTEYMENG 720
NOV2 : 721 LDTFLRTHDGQFTIMQLVGMLRGVGAGMRYLSDLGYVHRDLAARNVLVDSNLVCKVSDFG 780
|||||
Sbjct: 721 LDTFLRTHDGQFTIMQLVGMLRGVGAGMRYLSDLGYVHRDLAARNVLVDSNLVCKVSDFG 780
NOV2 : 781 LSRVLEDDPDAAAYTTTGGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 840
|||||
Sbjct: 781 LSRVLEDDPDAAAYTTTGGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 840
NOV2 : 841 NMTNRDVISSVEEGYRLPAPMGCPHALHQLMLDCWHKDRAQRPRFSQIVSVLDALIRSPE 900
|||||
Sbjct: 841 NMTNRDVISSVEEGYRLPAPMGCPHALHQLMLDCWHKDRAQRPRFSQIVSVLDALIRSPE 900
NOV2 : 901 SLRATATVSRCPPPAFVRSCFDLRGGSGGGGGLTVGDWLDSIRMGRYRDHFAAGGYSSLG 960
|||||
Sbjct: 901 SLRATATVSRCPPPAFVRSCFDLRGGSGGGGGLTVGDWLDSIRMGRYRDHFAAGGYSSLG 960
NOV2 : 961 MVLRMNAQDVRLGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:5)
|||||
Sbjct: 961 MVLRMNAQDVRLGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:53)

On page 16, kindly replace the paragraph in Table 7 beginning at line 4 with the following:

A⁶
Table 7 shows multiple sequence alignment of the NOV2 ephrin type-A receptor 8-like protein of the invention, shown as AL035703 Spliced2, with similar proteins. The various aligned proteins are as follows: AL035703 Spliced2 (SEQ ID NO:5) with several proteins: EPA8 Mouse (SEQ ID NO:54), EPA5 Human (SEQ ID NO:55) and EPA5 Chick (SEQ ID NO:56). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

On page 20, please replace the paragraph in Table 9 beginning at line 5 with the following:

A⁷
Table 9 shows sequence alignment between a NOV3 polypeptide with several members of the human fibronectin leucine repeat transmembrane family: AAF28461.1|AF169 (SEQ ID NO:57), AAF28460.1|AF169 (SEQ ID NO:58) and AAF28459.1|AF169 (SEQ ID NO:59). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

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On page 21, kindly replace Table 9. continued with the following Table 9A:

TABLE 9A.

```
>ref|NP_037412.1| fibronectin leucine rich transmembrane protein 1
gb|AAF28459.1|AF169675_1 (AF169675) leucine-rich repeat transmembrane protein FLRT1
[Homo
      sapiens]
Length = 674
```

Score = 1365 bits (3494), Expect = 0.0
Identities = 673/674 (99%), Positives = 674/674 (99%)

NOV3:	1	MVVAHPTATATTTPTATVTATVVMTTATMDLRDWFLLFCYGLIAFLTEVIDSTTCPSVCRC	60
Sbjct:	1	MVVAHPTATATTTPTATVTATVVMTTATMDLRDWFLLFCYGLIAFLTEVIDSTTCPSVCRC	60
NOV3:	61	DNGFIYCNDRGLTSPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDE	120
Sbjct:	61	DNGFIYCNDRGLTSPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDE	120
NOV3:	121	FPINLPRSLRELHLQDNNVRTIARDSLARIPPLEKLHLDDNSVSTVSI EEDAFADSKQLK	180
Sbjct:	121	FPINLPRSLRELHLQDNNVRTIARDSLARIPPLEKLHLDDNSVSTVSI EEDAFADSKQLK	180
NOV3:	181	LLFLSRNHLSSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIA	240
Sbjct:	181	LLFLSRNHLSSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIA	240
NOV3:	241	DDTFSRLQNLTELSLVRNSLAAPPLNLP SAHLQKLYLQDNAISHIPYNTLAKMRELERLD	300
Sbjct:	241	DDTFSRLQNLTELSLVRNSLAAPPLNLP SAHLQKLYLQDNAISHIPYNTLAKMRELERLD	300
NOV3:	301	LSNNNLTTLPRGLFDDLGNLAQLLRNNPWF CGCNLMWLRDWVKARA AVNVNVRGLMCQGP	360
Sbjct:	301	LSNNNLTTLPRGLFDDLGNLAQLLRNNPWF CGCNLMWLRDWVKARA AVNVNVRGLMCQGP	360
NOV3:	361	EKVRGMAIKDITSEMDEC FETGPQGGVANAAAKTTASNHASATTPQGS LFTLAKRPGLR	420
Sbjct:	361	EKVRGMAIKDITSEMDEC FETGPQGGVANAAAKTTASNHASATTPQGS LFTLAKRPGLR	420
NOV3:	421	LPDSNIDYPMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLGHSPAVGSI	480
Sbjct:	421	LPDSNIDYPMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLGHSPAVGSI	480
NOV3:	481	TETLVQGDKTEYLLTALEPKSTYIICMVTMETS NAYVADETPVCAKAETADSYGPTTTLN	540
Sbjct:	481	TETLVQGDKTEYLLTALEPKSTYIICMVTMETS NAYVADETPVCAKAETADSYGPTTTLN	540
NOV3:	541	QEQNAGPMASLPLAGIIGGAVALVFLFVLGAICWYVHQAGELLTRERAYNRGSRKKDDY	600
Sbjct:	541	QEQNAGPMASLPLAGIIGGAVALVFLFVLGAICWYVHQAGELLTRERAYNRGSRKKDDY	600
NOV3:	601	MESGTTKDNSILEIRGPGLOMLPINPYRAKEEYVVHTIFPSNGSSLCKATHTIGYGTTRG	660
Sbjct:	601	MESGTTKDNSILEIRGPGLOMLPINPYRAKEEYVVHTIFPSNGSSLCKATHTIGYGTTRG	660
NOV3:	661	YRDGGIPDIDYSYT 674 (SEQ ID NO:7)	
Sbjct:	661	YRDGGIPDIDYSYT 674 (SEQ ID NO:60)	

On page 22, please replace the paragraph in Table 10 beginning at line 6 with the following: